

## Raw Sequence Listing Error Summary

### ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/981,649

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO.X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO.X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9 ✓ Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

## RAW SEQUENCE LISTING

DATE: 11/13/2001

PATENT APPLICATION: US/09/981,649

TIME: 10:33:44

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\11132001\I981649.raw

**Does Not Comply  
Corrected Diskette Needed**

2 <110> APPLICANT: Asundi, Vinod  
 3 Ford, John E.  
 4 Drmanac, Radoje T.  
 5 Liu, Chenghua  
 6 Tang, Y. Tom  
 7 Yamasaki, Vicky  
 8 Yeung, George  
 9 Zhang, Jie  
 10 Zhou, Ping  
 11 Zhou, Hua

W--> 12 <120> TITLE OF INVENTION: EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS  
 W--> 13 <130> FILE REFERENCE: 28110/37665  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/981,649  
 C--> 14 <141> CURRENT FILING DATE: 2001-10-15  
 14 <150> PRIOR APPLICATION NUMBER: US 09/687,860  
 15 <151> PRIOR FILING DATE: 2000-10-13  
 16 <150> PRIOR APPLICATION NUMBER: US 09/620,312  
 17 <151> PRIOR FILING DATE: 2000-07-19  
 18 <150> PRIOR APPLICATION NUMBER: US 09/363,316  
 19 <151> PRIOR FILING DATE: 1999-07-28

W--> 20 <160> NUMBER OF SEQ ID: 32  
 21 <170> SOFTWARE: FastSEQ for Windows Version 3.0

W--> 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 300  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens

W--> 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (1)...(300)  
 29 <221> NAME/KEY: misc\_feature  
 30 <222> LOCATION: (1)...(300)  
 31 <223> OTHER INFORMATION: n' = A,T,C or G

W--> 32 <400> SEQUENCE: 1

33	ggc tgg aga aga aac agc aag gga gtc tgt gaa gct aca tgc gaa cct	48
34	Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro	
35	1 5 10 15	
37	gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt	96
38	Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe	
39	20 25 30	
41	cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga	144
42	Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly	
43	35 40 45	
45	atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc	192
46	Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser	
47	50 55 60	
49	tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg	240
50	Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr	

The type of errors shown exist throughout  
 the Sequence Listing. Please check subsequent  
 sequences for similar errors.

see error summary sheet, Item 9

- explanation was not given for Xaa

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Input Set : A:\PTO.DC.txt

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```

51      65      70      75      80
W--> 53 tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt 288
W--> 54 Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
55                                     85                                     90                                     95
56 gaa gac aca gaa
57 Glu Asp Thr Glu
58                                     100
60 <210> SEQ ID NO: 2
61 <211> LENGTH: 1611
62 <212> TYPE: DNA
63 <213> ORGANISM: Homo sapiens
W--> 64 <220> FEATURE:
65 <221> NAME/KEY: CDS
66 <222> LOCATION: (1)...(1506)
67 <221> NAME/KEY: misc_feature
68 <222> LOCATION: (1)...(1611)
69 <223> OTHER INFORMATION: n = A,T,C or G
W--> 70 <400> SEQUENCE: 2
71 ggc tgg aga aga aac agc aag gga gtc tgt gaa gct aca tgc gaa cct 48
72 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
73 1 5 10 15
75 gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt 96
76 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
77 20 25 30
79 cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga 144
80 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
81 35 40 45
83 atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc 192
84 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
85 50 55 60
87 tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg 240
88 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
89 65 70 75 80
W--> 91 tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt 288
W--> 92 Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
93                                     85                                     90                                     95
95 gaa gac aca gaa gaa ggg cca cag tgc ctg tgt cca tcc tca gga etc 336
96 Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
97 100 105 110
99 cgc ctg gcc cca aat gga aga gac tgt cta gat att gat gaa tgt gcc 384
100 Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala
101 115 120 125
103 tct ggt aaa gtc atc tgt ccc tac aat cga aga tgt gtg aac aca ttt 432
104 Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe
105 130 135 140
106 gga agc tac tac tgc aaa tgt cac att ggt ttc gaa ctg caa tat atc 480
107 Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile
108 145 150 155 160
110 agt gga cga tat gac tgt ata gat ata aat gaa tgt act atg gat agc 528

```

*- same error*

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```

111 Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser
112                               165                               170                               175
114 cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc      576
115 His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe
116                               180                               185                               190
118 aag tgt aaa tgc aag cag gga tat aaa ggc aat gga ctt cgg tgt tct      624
119 Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser
120                               195                               200                               205
122 gct atc cct gaa aat tct gtg aag gaa gtc ctc aga gca cct ggt acc      672
123 Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr
124                               210                               215                               220
126 atc aaa gac aga atc aag aag ttg ctt gct cac aaa aac agc atg aaa      720
127 Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys
128                               225                               230                               235
130 aag aag gca aaa att aaa aat gtt acc cca gaa ccc acc agg act cct      768
131 Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro
132                               245                               250                               255
134 acc cct aag gtg aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc      816
135 Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser
136                               260                               265                               270
138 aga ggc ggg aac tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg      864
139 Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met
140                               275                               280                               285
142 aaa gag ggg ctt gag gat gag aaa aga gaa gag aaa gcc ctg aag aat      912
143 Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn
144                               290                               295                               300
146 gac ata gag gag cga agc ctg cga gga gat gtg ttt ttc cct aag gtg      960
147 Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val
148                               305                               310                               315
150 aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta      1008
151 Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu
152                               325                               330                               335
154 act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc      1056
155 Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser
156                               340                               345                               350
158 ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt      1104
159 Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe
160                               355                               360                               365
161 gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca      1152
162 Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala
163                               370                               375                               380
165 gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt      1200
166 Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu
167                               385                               390                               395
169 ctg cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat      1248
170 Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp
171                               405                               410                               415
173 tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa      1296
174 Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys

```

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```

175          420          425          430
177 aac agt aac aat gcc ctg gca tgg gag aag acc acg agt gag gat gaa 1344
178 Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu
179          435          440          445
181 aag tgg aag aca ggg aaa att cag ttg tat caa gga act gat gct acc 1392
182 Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr
183          450          455          460
185 aaa agc atc att ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa 1440
186 Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
187          465          470          475          480
189 atc gca gtg gat ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc 1488
190 Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser
191          485          490          495
W--> 193 ctt tta tct gtg gan nnc tgaatgggtac tatctttata ttgactttg 1536
W--> 194 Leu Leu Ser Val Xaa' Xaa Some error
195          500
197 tatgtcaagtt cctcgtgtttt ttgatattg catcatagga cctctggcat tttaaaatta 1596
198 ctactgtgaaa aattg 1611
199 <210> SEQ ID NO: 3
200 <211> LENGTH: 100
201 <212> TYPE: PRT
202 <213> ORGANISM: Homo sapiens
W--> 203 <400> SEQUENCE: 3
204 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
205 1 5 10 15
206 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
207 20 25 30
208 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
209 35 40 45
210 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
211 50 55 60
212 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
213 65 70 75 80
214 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
215 85 90 95
216 Glu Asp Thr Glu
217 100
218 <210> SEQ ID NO: 4
219 <211> LENGTH: 537
220 <212> TYPE: PRT
221 <213> ORGANISM: Homo sapiens
W--> 222 <220> FEATURE:
223 <221> NAME/KEY: VARIANT
224 <222> LOCATION: (1)...(537)
225 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 226 <400> SEQUENCE: 4
227 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
228 1 5 10 15
230 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe

```

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```

231          20          25          30
232 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
233          35          40          45
234 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
235          50          55          60
236 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
237          65          70          75          80
238 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
239          85          90          95
240 Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
241          100          105          110
242 Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala
243          115          120          125
244 Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe
245          130          135          140
246 Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile
247          145          150          155          160
248 Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser
249          165          170          175
250 His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe
251          180          185          190
252 Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser
253          195          200          205
254 Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr
255          210          215          220
256 Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys
257          225          230          235          240
258 Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro
259          245          250          255
260 Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser
261          260          265          270
262 Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met
263          275          280          285
264 Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn
265          290          295          300
266 Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val
267          305          310          315          320
268 Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu
269          325          330          335
270 Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser
271          340          345          350
272 Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe
273          355          360          365
274 Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala
275          370          375          380
276 Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu
277          385          390          395          400
278 Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp
279          405          410          415
280

```

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Input Set : A:\PTO.DC.txt

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L:12 M:283 W: Missing Blank Line separator, <120> field identifier  
L:13 M:283 W: Missing Blank Line separator, <130> field identifier  
L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:20 M:283 W: Missing Blank Line separator, <160> field identifier  
L:22 M:283 W: Missing Blank Line separator, <210> field identifier  
L:26 M:283 W: Missing Blank Line separator, <220> field identifier  
L:32 M:283 W: Missing Blank Line separator, <400> field identifier  
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:64 M:283 W: Missing Blank Line separator, <220> field identifier  
L:70 M:283 W: Missing Blank Line separator, <400> field identifier  
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:203 M:283 W: Missing Blank Line separator, <400> field identifier  
L:222 M:283 W: Missing Blank Line separator, <220> field identifier  
L:226 M:283 W: Missing Blank Line separator, <400> field identifier  
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:302 M:283 W: Missing Blank Line separator, <220> field identifier  
L:305 M:283 W: Missing Blank Line separator, <400> field identifier  
L:396 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:462 M:283 W: Missing Blank Line separator, <220> field identifier  
L:466 M:283 W: Missing Blank Line separator, <400> field identifier  
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:542 M:283 W: Missing Blank Line separator, <220> field identifier  
L:546 M:283 W: Missing Blank Line separator, <400> field identifier.  
L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:557 M:283 W: Missing Blank Line separator, <220> field identifier  
L:561 M:283 W: Missing Blank Line separator, <400> field identifier  
L:562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:572 M:283 W: Missing Blank Line separator, <400> field identifier  
L:599 M:283 W: Missing Blank Line separator, <220> field identifier  
L:603 M:283 W: Missing Blank Line separator, <400> field identifier  
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:614 M:283 W: Missing Blank Line separator, <220> field identifier  
L:618 M:283 W: Missing Blank Line separator, <400> field identifier  
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:631 M:283 W: Missing Blank Line separator, <220> field identifier

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Input Set : A:\PTO.DC.txt

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L:633 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:639 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:641 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:647 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:649 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:655 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:657 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:663 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:665 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:671 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:673 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:679 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:683 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
 L:752 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:754 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:760 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:762 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:768 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:778 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:788 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:791 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:913 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:992 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:994 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1001 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:1017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
 L:1025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1028 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1031 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1034 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1040 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1043 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1046 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1049 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1052 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1055 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1058 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1064 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1067 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1071 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1074 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1077 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1080 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1083 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1086 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1089 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27



## VERIFICATION SUMMARY

DATE: 11/13/2001

PATENT APPLICATION: US/09/981,649

TIME: 10:33:45

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\11132001\I981649.raw

L:1092 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1095 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1098 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1122 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:1232 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1244 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1250 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29

OIEP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/981,649

DATE: 11/02/2001

TIME: 15:12:26

Input Set : A:\37665seq.txt

Output Set: N:\CRF3\11022001\I981649.raw

**Does Not Comply  
Corrected Diskette Needed**

2 <110> APPLICANT: Asundi, Vinod  
 3 Ford, John E.  
 4 Drmanac, Radoje T.  
 5 Liu, Chenghua  
 6 Tang, Y. Tom  
 7 Yamasaki, Vicky  
 8 Yeung, George  
 9 Zhang, Jie  
 10 Zhou, Ping  
 11 Zhou, Hua

W--> 12 <120> TITLE OF INVENTION: EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS  
 W--> 13 <130> FILE REFERENCE: 28110/37665  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/981,649  
 C--> 14 <141> CURRENT FILING DATE: 2001-10-15  
 14 <150> PRIOR APPLICATION NUMBER: US 09/687,860  
 15 <151> PRIOR FILING DATE: 2000-10-13  
 16 <150> PRIOR APPLICATION NUMBER: US 09/620,312  
 17 <151> PRIOR FILING DATE: 2000-07-19  
 18 <150> PRIOR APPLICATION NUMBER: US 09/363,316  
 19 <151> PRIOR FILING DATE: 1999-07-28

W--> 20 <160> NUMBER OF SEQ ID: 32  
 21 <170> SOFTWARE: FastSEQ for Windows Version 3.0

## ERRORED SEQUENCES

772 <210> SEQ ID NO: 22  
 773 <211> LENGTH: 20  
 774 <212> TYPE: DNA  
 775 <213> ORGANISM: Artificial Sequence

W--> 776 <220> FEATURE:  
 777 <223> OTHER INFORMATION: Description of Artificial Sequence: primer

W--> 778 <400> SEQUENCE: 22  
 E--> 779 gggaactgac atacaagtc



22 <sup>must be</sup> ~~was~~ added at the end of the line  
 (no. of nucleotides)

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/981,649

DATE: 11/02/2001

TIME: 15:12:27

Input Set : A:\37665seq.txt

Output Set: N:\CRF3\11022001\I981649.raw

L:12 M:283 W: Missing Blank Line separator, <120> field identifier  
L:13 M:283 W: Missing Blank Line separator, <130> field identifier  
L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:20 M:283 W: Missing Blank Line separator, <160> field identifier  
L:22 M:283 W: Missing Blank Line separator, <210> field identifier  
L:26 M:283 W: Missing Blank Line separator, <220> field identifier  
L:32 M:283 W: Missing Blank Line separator, <400> field identifier  
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:64 M:283 W: Missing Blank Line separator, <220> field identifier  
L:70 M:283 W: Missing Blank Line separator, <400> field identifier  
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:203 M:283 W: Missing Blank Line separator, <400> field identifier  
L:222 M:283 W: Missing Blank Line separator, <220> field identifier  
L:226 M:283 W: Missing Blank Line separator, <400> field identifier  
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:302 M:283 W: Missing Blank Line separator, <220> field identifier  
L:305 M:283 W: Missing Blank Line separator, <400> field identifier  
L:396 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:462 M:283 W: Missing Blank Line separator, <220> field identifier  
L:466 M:283 W: Missing Blank Line separator, <400> field identifier  
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:542 M:283 W: Missing Blank Line separator, <220> field identifier  
L:546 M:283 W: Missing Blank Line separator, <400> field identifier  
L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:557 M:283 W: Missing Blank Line separator, <220> field identifier  
L:561 M:283 W: Missing Blank Line separator, <400> field identifier  
L:562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:572 M:283 W: Missing Blank Line separator, <400> field identifier  
L:599 M:283 W: Missing Blank Line separator, <220> field identifier  
L:603 M:283 W: Missing Blank Line separator, <400> field identifier  
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:614 M:283 W: Missing Blank Line separator, <220> field identifier  
L:618 M:283 W: Missing Blank Line separator, <400> field identifier  
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:631 M:283 W: Missing Blank Line separator, <220> field identifier

## VERIFICATION SUMMARY

DATE: 11/02/2001

PATENT APPLICATION: US/09/981,649

TIME: 15:12:27

Input Set : A:\37665seq.txt

Output Set: N:\CRF3\11022001\I981649.raw

L:633 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:639 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:641 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:647 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:649 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:655 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:657 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:663 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:665 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:671 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:673 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:679 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:683 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
 L:752 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:754 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:760 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:762 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:768 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:770 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:776 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:778 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:779 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:22  
 L:784 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:787 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:909 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:988 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:1013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
 L:1021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1024 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1027 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1030 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1033 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1036 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1039 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1042 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1048 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1051 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1054 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1060 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1063 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1067 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1070 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1073 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1076 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1079 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
 L:1082 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/981,649

DATE: 11/02/2001

TIME: 15:12:27

Input Set : A:\37665seq.txt

Output Set: N:\CRF3\11022001\I981649.raw

L:1085 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1088 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1091 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1094 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1097 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1100 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27  
L:1220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:1228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1231 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1234 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1240 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1243 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1252 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1258 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:1267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29